

CGACACCCTT GGAGAGGIGC GCGIGCTIGA GICGGIIGCI AAAGACIAIC TAAAAACCCT CAAACIGGIC ICIACGIICC CCACTICCIC GCGAAGGAIG GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG ATTTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCC

101 CGTTAGGGAA CTCTGGGGAC AGAGCGCCCC GGCCGCCTGA TGCCCGAGGC AGGTGCGAC CCAGGACCCA GGACGGCGTC GGAACCATA CCATGGCCCG GCAATCCCIT GAGACCCCIG ICICGCGGGG CCGGCGGACT ACCGGCTCCG ICCCACGCTG GGTCCTGGGT CCTGCCGCAG CCCTTGGTAT GGTACCGGGC

Metalaarg

CTAGGGGTTC TGGGATTTCA AGCAGCAGCA GTAGCAGCGC CAGGACGACG GTCAGGATCG AATGAGACGG TGGTGACGGG CCGTCCTCCT TCAAGGGGTC ThrLeuLysp hevalvalva lilevalAla ValLeuLeuP roValLeuAl aTyrSerAla ThrThrAlaA rgGlnGluGl uValProGln 201 GATCCCCAAG ACCTAAAGT TCGTCGTCGTCGTCGTCGCG GTCCTGCTGC CAGTCCTAGC TTACTCTGCC ACCACTGCCC GGCAGGAGGA AGTTCCCCAG IleProLys

GINTHEVALA LAPROGINGI NGINARGHIS SERPHELYSG LYGINGINCY SPROALAGLY SERHISARGS ERGINHISTH RGLYALACYS ASNPROCYSTHR GICIGICACO GGGGIGICGI IGICICCGIG ICGAAGIICO CCCICCICAO AGGICGICCI AGAGIAICIA GICIIGIAIG ACCICGGACA IIGGGCACGI 301 CAGACAGIGG CCCCACAGCA ACAGAGGCAC AGCITCAAGG GGGAGGAGIG ICCAGCAGGA ICICAÍAGAI CAGAACAIAC IGGAGCCIGI AACCCGIGCA 37 401 CAGAGGGTGT GGATTACACC AACGCTTCCA ACAATGAACC TTCTTGCTTC CCATGTACAG TTTGTAAATC AGATCAAAAA CATAAAAGTT CCTGCACCAT CCIAAIGIGG INGCGAAGGI IGITACINGG AAGAACGAAG GGIACAIGIC AAACAITIAG ICIAGITITI GIAITITICAA GGACGIGGIA

Gluglyva laspTyrThr AsnAlaSerA snAsnGluPr oSerCysPhe ProCysThrV alCysLysSe rAspGlnLys HisLysSerS erCysThrMet

501 GACCAGAGAC ACAGTGTGT AGTGTAAAGA AGGCACCTTC CGGAATGAAA ACTCCCCAGA GATGTGCGG AAGTGTAGCA GGTGCCCTAG TGGGGAAGTAA TGTCACACAG TCACATTICT TCCGTGGAAG GCCTTACTIT TGAGGGGTCT CTACACGGCC TTCACATGGT CCACGGGATC ACCCCTTQAG Thraigasp ThrvalcysG incysLysG1 uGlyThrPhe ArgasnGlua snSerProG1 uMetCysArg LysCysSerA rgCysProSe rGlyGlu CTGGTCTCTG 104

SEP 2 0 2001

Glnvalsera sncysThrSe rTrpAspAsp IleGlnCysV alGluGluPh eGlyAlaAsn AlaThrValG luThrProAl aAlaGluGlu ThrMetAsnThr 601 CAAGTCAGTA ATTGTACGTC CTGGGATGAT ATCCAGTGTG TTGAAGAATT TGGTGCCAAT GCCACTGTGG AAACCCCAGC TGCTGAAGAG ACAATGAAÖ GITCAGICAT TAACAIGCAG GACCCIACIA IAGGICACAC AACTICITAA ACCACGGITA CGGIGACACC ITIGGGGICG ACGACITCIC 137

GGTCGGGCCC CTGAGGACGG GGTCGACGAC TICICIGITA CITGTGGTCG GGTCCCTGAG GACGGGGTCG ACGACTICIC IGITACTGGT GGTCGGGCCC 701 CCAGCCCGGG GACTCCTGCC CCAGCTGCTG AAGAGACAAT GAACACCAGC CCAGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCGGG

SerProGl yThrProAla ProAlaAlaG luGluThrMe tAsnThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProGly 171

FIG._1A-1



- 801 GACTCCTGCC CCAGCTGCTG AAGAGACAAT GACCACCAGC CCGGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCGGG GACTCCTGCC CTGAGGACGG GGTCGACGAC TICTCTGTTA CTGGTGGTCG GGCCCCTGAG GACGGGGTCG ACGACTTCTC TGTTACTGGT GGTCGGGCCC CTGAGGACGG ThrProAla ProAlaAlaG luGluThrMe tThrThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProGl yThrProAla 204
- TCITCICATI ACCICICAIG CACCAICGIA GGGATCAIAG ITCIAATIGI GCITCIGAIT GIGITIGITI GAAAGACITC ACTGIGGAAG AAATICCITIC AGAAGAGTAA TGGAGAGTAC GTGGTAGCAT CCCTAGTATC AAGATTAACA CGAAGACTAA CACAAACAAA CTTTCTGAAG TGACACCTTC TTTAAGGAAG 901
 - SerSerHisT yrLeuSerCy sThrIleVal GlyIleIleV alLeuIleVa lLeuLeuIle ValPheVal 237
- 1001 CITACCIGAA AGGITCAGGI AGGGGCIGGC IGAGGGCGGG GGGCGCIGGA CACICITGC CCIGCCICCC ICIGCIGIGI ICCCACAGAC AGAAACGCCI BARTGGACTT TECAAGTECA TECGEGACEG ACTECEGECE ECEGEGACET GTGAGACG GGACGGAGGG AGACGACACA AGGGTGTETG TETTTGEGGA
- 1101

FIG._ 1A-2

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- MetGlnGl yValLysGlu ArgPheLeuPro 1 GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG ATTTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC CGACACCCTT GGAGAGGTGC GCGTGCTTGA GTCGGTTGCT AAAGACTATC TAAAAACCCT CAAACTGGTC TCTACGTTCC CCACTTCCTC GCGAAGGATG -40
- LeuGlyAs nSerGlyAsp ArgAlaProA rgProProAs pGlyArgGly ArgValArgP roArgThrG1 nAspGlyVal GlyAsnHisT hrMetAlaArg 101 CGTTAGGGAA CTCTGGGGAC AGAGCGCCCC GGCCGCCTGA TGGCCGAGGC AGGGTGCGAC CCAGGACCCA GGACGGCGTC GGGAACCATA CCATGGCCCG GCAATCCCTT GAGACCCCTG TCTCGCGGGG CCGCCGGACT ACCGGCTCCG TCCCACGCTG GGTCCTGGGT CCTGCCGCAG CCCTTGGTAT GGTACCGGGC -30
- 201 GATCCCCAAG ACCTAAAGT TCGTCGTCGT CATCGTCGC GTCCTGCTGC CAGTCCTAGC TTACTCTGCC ACCACTGCCC GGCAGGAGGA AGTTCCCCAG CTAGGGGTTC TGGGATTTCA AGCAGCAGCA GTAGCAGCGC CAGGACGACG GTCAGGATCG AATGAGACGG TGGTGACGGG CCGTCCTCCT TCAAGGGGTC ThrLeuLyap hevalvalva lilevalala ValLeuLeuP rovalLeuAl aTyrSerAla ThrThrAlaA rgGlnGluGl uValProGln IleProLys
- GInThrvalk laprogingi nginkrgHis SerPheLysG lyGluGluCy sProklaGly SerHiskrgS erGluHisTh rGlyklaCys AsnProCysThr GICTGICACC GGGGTGICGI IGICICCGIG ICGAAGITCC CCCICCICAC AGGICGICCI AGAGIAICIA GICIIGIAIG ACCICGGACA IIGGGCACGI CAGACAGIGG CCCCACAGCA ACAGAGGCAC AGCITCAAGG GGGAGGAGIG TCCAGCAGGA TCTCATAGAT CAGAACATAC IGGAGCCTGT AACCCGTGCA 301 37

FIG._ 1B-1

Doomy or or a cont

- laspTyrThr AsnAlaSerA snAsnGluPr oSerCysPhe ProCysThrV alCysLysSe rAspGlnLys HisLysSerS erCysThrMet 401 CAGAGGGTGT GGATTACACC AACGCTTCCA ACAATGAACC TTCTTGCTTC CCATGTACAG TTTGTAAATC AGATCAAAAA CATAAAAGTT CCTGCACCAT CCTAATGTGG TTGCGAAGGT TGTTACTTGG AAGAACGAAG GGTACATGTC AAACATTTAG TCTAGTTTTT GTATTTTCAA GGACGTGGTA GluGlyVa GTCTCCCACA
- 501 GACCAGAGAC ACAGTGTGTC AGTGTAAAGA AGGCACCTTC CGGAATGAAA ACTCCCCAGA GATGTGCCGG AAGTGTAGCA GGTGCCCTAG TGGGGAAGTC CIGGICICIG IGICACACAG ICACATITCI ICCGIGGAAG GCCITACITI IGAGGGGICI CTACACGGCC IICACAICGI CCACGGGAIC ACCCCITCAG Thrargasp ThrvalcysG incysLysG1 uGlyThrPhe ArgasnGlua snSerProG1 uMetCysArg LysCysSerA rgCysProSe rGlyGluVal

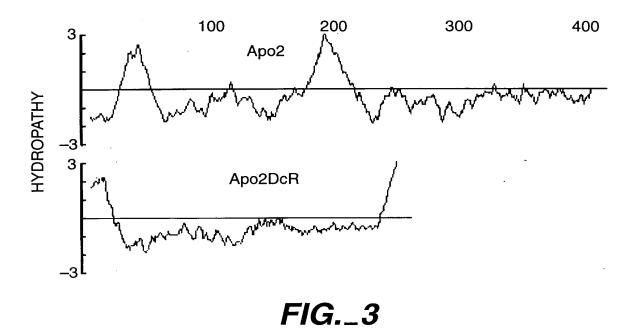
104

- TAGGICACAC AACTICITAA ACCACGGITA CGGIGACACC INTGGGGICG ACGACITCIC IGITACITGI 601 CAAGTCAGTA ATTGTACGTC CIGGGATGAT ATCCAGTGTG TTGAAGAATT TGGTGCCAAT GCCACTGTGG AAACCCCAGC TGCTGAAGAG ACAATGAACA GACCCTACTA TAACATGCAG GTTCAGTCAT
- GlnValSerA snCysThrSe rTrpAspAsp IleGlnCysV alGluGluPh eGlyAlaAsn AlaThrValG luThrProAl aAlaGluGlu ThrMetAsnThr 137
- 3 yThrProAla ProAlaAlaG luGluThrMe tAsnThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProGly GGICGGGCCC CIGAGGACGG GGICGACGAC TICICIGITA CIIGIGGICG GGICCCIGAG GACGGGGICG ACGACITCIC IGITACIGGI GGICGGCCC GACTCCTGCC CCAGCTGCTG AAGAGACAAT GAACACCAGC CCAGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCGGG CCAGCCCGGG SerProGl 701 171
- / 16 GACTCCTGCC CCAGCTGCTG AAGAGACAAT GACCACCAGC CCGGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCGGG GACTCCTGCC CIGAGGACGG GGICGACGAC TICICIGITA CIGGIGGICG GGCCCCIGAG GACGGGGICG ACGACIICIC IGIIACIGGI GGICGGGCCC CIGAGGACGG Thrprobla ProblablaG luGluThrMe tThrThrSer ProGlyThrP roblaProbl ablaGluGlu ThrMetThrT hrSerProGl yThrProbla 801 204
- TCTTCTCATT ACCTCTCATG CACCATCGTA GGGATCATAG TTCTAATTGT GCTTCTGATT GTGTTTGTTT GAAAGACTTC ACTGTGGAAG AAATTCCTTC CTTTCTGAAG TGACACCTTC TTTAAGGAAG AGAAGAGTAA TGGAGAGTAC GTGGTAGCAT CCCTAGTATC AAGATTAACA CGAAGACTAA CACAAACAAA yrLeuSerCy sThrIleVal GlyIleIleV alLeuIleVa lLeuLeuIle ValPheVal SerSerHisT
- CITACCIGAA AGGIICAGGI AGGCGCIGGC TGAGGGCGGG GGCGCIGGA CACICITCIGC CCIGCCICCC ICIGCIGIGI ICCCACAGAC AGAAACGCCI GAATGGACTT TCCAAGTCCA TCCGCGACCG ACTCCCGCCC CCCGCGACCT GTGAGAGAG GGACGGAGGG AGACGACACA AGGGTGTCTG TCTTTGCGGA 1001
- 1101 СССССТСССС СААРАРАРА ВАВАРАРА ВАРАРАРАЯ ВВРАРАРАЯ ВВРАРАРАЯ ВВРАРАРАРАЯ ВВРАРАРАЯ ВВРАРАРАЯ В

FIG._ 1B-2

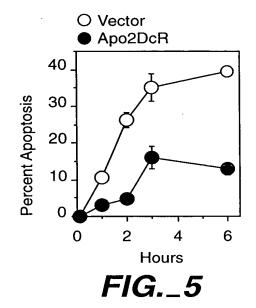
4/16

Apo2 Apo2DcR DR4	1 1 51	MEQRGQNAPAASGARKRHGPGPREARGARPGLRVPKTIVI MARIPKTLKFVV GRGALPTSMGQHGPSARARAGRAPGFRPAREASPRLRVHKTFKFVVVGVI
Apo2 Apo2DcR DR4	41 13 101	VVAAVLILVSAESALITQODLAPQQRAAPQOKRSSPSEGLCPPCHHISED VIVAVLIPVLAYSATTARQEEVPQOTVAPQOORHSFKGEFCPAGSHRSEH LQVVPSSAATIKLHDQSIGTQQWEHSPLGELCPPGSHRSER
Apo2 Apo2DcR DR4	91 63 142	CRD1 GRDCISCKYGODYSTHWNDLLFCLRCTRCDSGEVELSPCTTTRNTVCOCE TGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCK PGACNRCTEGVGYTNASNNLFACLPCTACKSDEPERSPCTTTRNTACQCK
Apo2 Apo2DcR DR4	141 113 192	CRD2 EGTFREEDSPEMCRKCRTGCPRGMVKVGDCTPWSDIECVHKE EGTFRNENSPEMCRKCSR-CPSGEVQVSNCTSWDDIQCVE-EFGANATVE PGTFRNDNSAEMCRKCSTGCPRGMVKVKDCTPWSDIECVHKE
Apo2 Apo2DcR DR4	161	TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAE
Apo2 Apo2DcR DR4	183 211 234	SGITIGVTVAAVVLIVAVFV ETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLIVLIVFVSGNGHNIWVILVVTLVVPILIVAV-LIVC
Apo2 DR4	203 262	CKSLLWKKVLPYLKGICSGGGDPERVDRSSQRPGAEDNVLNEIVSILQP CCIGSGCGGDPKCMDRVCFWRLGLLRGPGAEDNAHNEILSNADSLSTFVS
Apo2 DR4	253 312	TQVPEOFMEVQEPAEFTGVNMISPGESEHLLEPAEAERSQRRRLLVPANEEQQMESQEPADLTGVTVQSPGEAQCLLGPAEAEGSQRRRLLVPANG * **
Apo2 DR4 Apo3/DR3 TNFR1 CD95	303 358 338 322 220	GDPTETIRQCFDDFADIVPFDSWEPLMRKLGIMDNEI KVAKAEAAGH - R ADPTETIMLFFDKFANIVPFDSWDQLMRQLDLTKNEI DVVRAGTAGP - G VMDAVPARRWKEFVRTLGLREAEIEAVEVEI - GRF - R VVENVPPLRWKEFVRRLGLSDHEI DRIELQN - GRCLR IAGVHTLSQVKGFVRKNGVNEAKIDEIKNDN - VQDTA
Apo2 DR4 Apo3/DR3 TNFR1	351 406 374 358	* DILYTMLIKWVNKTGR-DASVHTLLDALETIGERLAKOKIEDHLLSSGKF DALYAMIMKWVNKTGR-NASIHTLLDALERMEERHAKEKIQDLLVDSGKF DQDYEMIKRWRQQQPAGLGAVYAALERMGLDGCVEDLRS EAQYSMIATWRRRTERREATLEILGRVLRDMDLLGCLEDIEE
CD95 Apo2 DR4	256 400 455	MYLEGNADSALS



Gontrol PI-PLC P

FIG._4



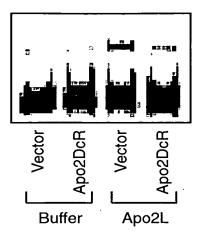


FIG._6

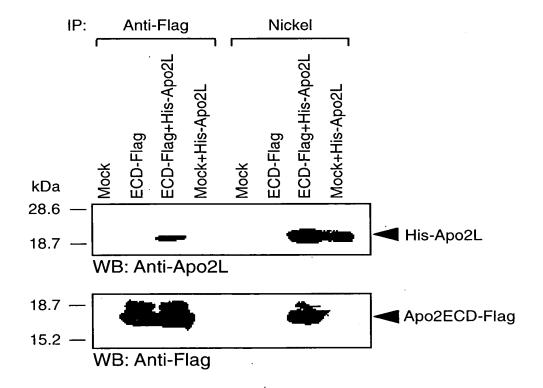
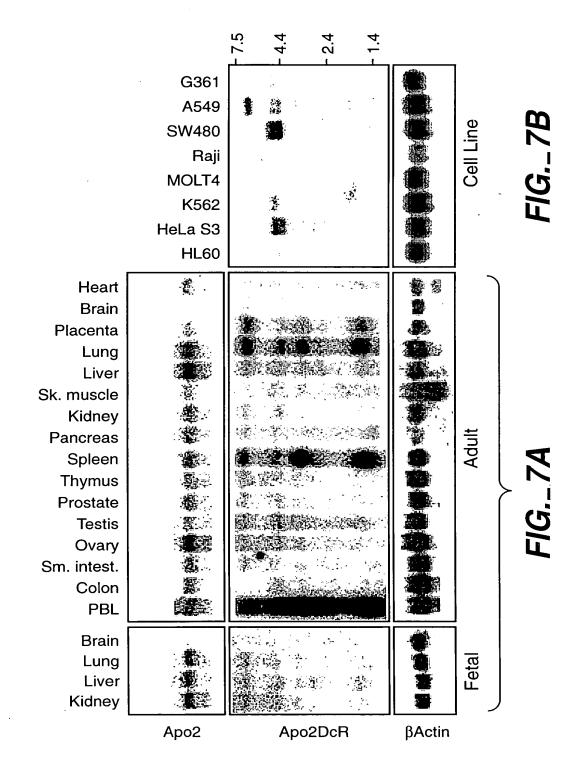


FIG._10



DEADERS OBECOL

GAGAACCC CGCAATCTCT GCGCCCACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC	CTCTTGGG GCGTTAGAGA CGCGGGTGTT TTATGTGGCT GCTACGGGCT AGATGAAATT CCCGACTTTG
J.	AG.
CGATGCCCGA	GCTACGGGCJ
AATACACCGA	TTATGTGGCT
GCCCCACAA	CGCGGGTGTT
CGCAATCTCT	GCGTTAGAGA
CGGAGAACCC	GCCTCTTGGG
AGCACGCGGC	TCGTGCGCCG
CGCATAAATC	GGGTGCGCAG GCGTATTTAG TCGTGCGCCG GCC
1 CCCACGCGTC CGCATAAATC AGCACGCGGC CGGA	GGGTGCGCAG

etGluGlnAr gGlyGlnAsn AlaProAlaA laSerGlyAl aArgLysArg HisGlyProGly 101 CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCCA TGGAACAACG GGGACAGAAC GCCCCGGCCG CTTCGGGGGG CCGGAAAAGG CACGGCCCAG GGTGCCCGGA CTCTCTGATA TTCTCGCAAG GGATGGCGGT ACCTTGTTGC CCCTGTCTTG CGGGCCGGG GAAGCCCCCG GGCCTTTTCC GTGCCGGGTC

ProArgGl uAlaArgGly AlaArgProG lyLeuArgVa lProLysThr LeuValLeuV alValAlaAl aValLeuLeu LeuValSerA laGluSerAla 201 GACCCAGGGA GGCGGGGGA GCCAGGCCTG GGCTCCGGGT CCCCAAGACC CTTGTGCTCG TTGTCGCCGC GGTCCTGCTG TTGGTCTCAG CTGAGTCTGC GACTCAGACG CTGGGTCCCT CCGCGCCCCT CGGTCCGGAC CCGAGGCCCA GGGGTTCTGG GAACACGAGC AACAGCGGCG CCAGGACGAC AACCAGAGTC 22

301 TCTGATCACC CAACAAGACC TAGCTCCCCA GCAGAGAGGG GCCCCACAAC AAAAGAGGTC CAGCCCCTCA GAGGGATTGT GTCCACCTGG ACACCATATC LeuIleThr GinGlnAspL euAlaProGl nGlnArgAla AlaProGinG inLysArgSe rSerProSer GiuGlyLeuC ysProProGl yHisHisile TTTTCTCCAG GTCGGGGAGT CTCCCTAACA CAGGTGGACC AGACTAGIGG GIIGITCIGG AICGAGGGGI CGICICICGC CGGGGIGIIG

16 8 / SerGluAspG lyArgAspCy sIleSerCys LysTyrGlyG lnAspTyrSe rThrHisTrp AsnAspLeuL euPheCysLe uArgCysThr ArgCysAspSer AGTOTTOTGO CATOTOTANO GINGAGGACG TITATACCTG TCCTGATATO GIGAGTGACC TTACTGGAGG AAAAGACGAA CGCGACGTGG TCCACACTAA TCAGAAGACG GTAGAGATTG CATCTCCTGC AAATATGGAC AGGACTATAG CACTCACTGG AATGACCTCC TTTTCTGCTT GCGCTGCACC AGGTGTGATT 401

GlyGluVa lGluLeuSer ProCysThrT hrThrArgAs nThrValCys GlnCysGluG luGlyThrPh eArgGluGlu AspSerProG luMetCysArg CCTCGATTCA GGGACGTGGT GCTGGTCTTT GTGTCACACA GTCACGCTTC TTCCGTGGAA GGCCCTTCTT CTAAGAGGAC TCTACACGGC CAGGTGAAGT GGAGCTAAGT CCCTGCACCA CGACCAGAAA CACAGTGTGT CAGTGCGAAG AAGGCACCTT CCGGGAAGAA GATTCTCCTG AGATGTGCCG GTCCACTTCA 501 122

TGTCCCACAG GGTCTCCCTA CCAGTTCCAG CCACTAACAT GTGGGACCTC ACTGTAGCTT ACACAGGTGT TTCTTAGTCC GTAGTAGTAT ThrGlyCysP roArgGlyMe tValLysVal GlyAspCysT hrProTrpSe rAspIleGlu CysValHisL ysGluSerGl yIleIlelle GAAGTGCCGC ACAGGGTGTC CCAGAGGGAT GGTCAAGGTC GGTGATTGTA CACCCTGGAG TGACATCGAA TGTGTCCACA AAGAATCAGG CATCATCATA CTTCACGGCG LysCysArg 109 155

CCTCAGTGTC AACGTCGGCA TCAGAACTAA CACCGACACA AACAAACGTT CAGAAATGAC ACCTTCTTTC AGGAAGGAAT GGACTTTCCG TAGACGAGTC GGAGTCACAG TIGCAGCCGI AGICTIGATI GIGGCIGIGI ITGITIGCAA GICITIACIG IGGAAGAAAG ICCITCCITA CCIGAAAGGC AICTGCICAG GlyValThrV alAlaAlaVa lValLeulle ValAlaValP heValCysLy sSerLeuLeu TrpLysLysV alLeuProTy rLeuLysGly 701

FIG._8A-1

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GlyGlyGl yAspProGlu ArgValAspA rgSerSerGl nArgProGly AlaGluAspA snValLeuAs nGluIleVal SerIleLeuG lnProThrGln CACCACCACC CCTGGGACTC GCACACCTGT CTTCGAGTGT TGCTGGACCC CGACTCCTGT TACAGGAGTT ACTCTAGCAC TCATAGAACG TCGGGTGGGT 801 GIGGIGGIGG GGACCCIGAG CGIGIGGACA GAAGCICACA ACGACCIGGG GCIGAGGACA AIGICCICAA IGAGAICGIG AGIAICIIGC AGCĊCACCA 222

9 / ValProGlu GlnGluMetG luValGlnGl uProAlaGlu ProThrGlyV alAsnMetLe uSerProGly GluSerGluH isLeuLeuGl uProAlaGlu 901 GGTCCCTGAG CAGGAAATGG AAGTCCAGGA GCCAGCAGAG CCAACAGGTG TCAACATGTT GTCCCCCGGG GAGTCAGAGC ATCTGCTGGA ACCGGCAGAA CCAGGGACTC GTCCTTTACC TTCAGGTCCT CGGTCGTCTC GGTTGTCCCAC AGTTGTACAA CAGGGGGCCC CTCAGTCTCG TAGACGACCT TGGCCGTCTT 255

16 288 AlaGluArgS erGlnArgAr gArgLeuLeu ValProAlaA snGluGlyAs pProThrGlu ThrLeuArgG lnCysPheAs pAspPheAla AspLeuValPro 1001 GCTGAAAGGT CTCAGAGGAG GAGGCTGCTG GTTCCAGCAA ATGAAGGTGA TCCCACTGAG ACTCTGAGAC AGTGCTTCGA TGACTTTGCA GACTTGGTGC CGACITICCA GAGICICCIC CICCGACGAC. CAAGGICGII IACIICCACI AGGGIGACIC IGAGACITG ICACGAAGCI ACIGAAACGI CIGAACCACG

FIG._8A-2

TOCEO" 6/8/9860

spThrLeuTyr 1101 CCTTTGACTC CTGGGAGCCG CTCATGAGGA AGTTGGGCCT CATGGACAAT GAGATAAAGG TGGCTAAAGC TGAGGCAGGG GGCCACAGGG ACACCTTGTA GGAAACTGAG GACCCTCGGC GAGTACTCCT TCAACCCGGA GTACCTGTTA CTCTATTTCC ACCGATTTCG ACTCCGTCGC CCGGTGTCCC rTrpGluPro LeuMetArgL ysLeuGlyLe uMetAspAsn GluIleLysV alAlaLysAl aGluAlaAla GlyHisArgA 322

TCAACAAAAC CGGGCGAGAT GCCTCTGTCC ACACCCTGCT GGATGCCTTG GAGACGCTGG GAGAGAGAT TGCCAAGCAG GICCIACGAC IAITICACCC AGIIGITITIG GCCGCICIA CGGAGACAGG IGIGGGACGA CCIACGGAAC CICIGCGACC CICICICIGA ACGGIICGIC CACGATGCTG ATAAAGTGGG 1201

ThrMetLeu IleLysTrpV alAsnLysTh rGlyArgAsp AlaSerValH isThrLeuLe uAspAlaLeu GluThrLeuG lyGluArgLe uAlaLysGln

TICINACTIC TEGIGAACNA CTCGAGACCI TTCANGIACA TAGATCITCC ATTACGICTG AGACGGAACA GGATTCACAC TAAGAGAAGT CCTTCACTCT 1301 AAGATTGAGG ACCACTTGTT GAGCTCTGGA AAGTTCATGT ATCTAGAAGG TAATGCAGAC TCTGCCWTGT CCTAAGTGTG ATTCTCTTCA GGAAGTGAGA userserGly LysPheMetT yrLeuGluGl yAsnAlaAsp SerAlaXqqS erOC* spHisLeuLe LysileGluA

10 SGAAGGGACC AAATGGAAAA AAGACCTTTT TCGGGTTGAC CTGAGGTCAG TCATCCTTTC ACGGTGTAA CAGTGTACTG GCCATGACCT TCTTTGAGAG TICTGGAAAA AGCCCAACTG GACTCCAGTC AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC TTTACCTTTT CCTTCCCTGG 1401

/ 16 CTATGGAAAT TTATTCCTGT GATACCTTTA AATAAGGACA CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACTT TTCACTGCAC TTGGCATTAT TTTTATAAGC TGAATGTGAT CTACCTIGIA GGACATIGAA AAGIGACGIG AACCGIAATA AAAATATICG ACITACACIA AGTGGGTCAC 1501

TICCGITICI GCGIACITIC AGAITIGGIT IGGGAIGICA INGITITCAC AGCACITITI TAICCIAAIG IAAAIGCITI AITIAITIAI CAGACCTAGT AAGGCAAACA CGCATGAAAC TCTAAACCAA ACCCTACAGT AACAAAAGTG TCGTGAAAAA ATAGGATTAC ATTTACGAAA TAAATAAATA GTCTGGATCA

AACCCGATGT AACATTCTAG GTAGATGTTT TITITITIT ITTTTTTTC CCGCCGCGC TGAGATCTCA GCTGGACGTC TTCGAACCGG CGGTACCGG 1701 ITGGGCTACA ITGTAAGATC CATCTACAAA AAAAAAAAA AAAAAAAAG GGCGGCGGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC

MEORGONA PAA SGARKRHGPGPREARGARPGLRVPKTLVLVVAAVLLLVSAESAL ITQOD

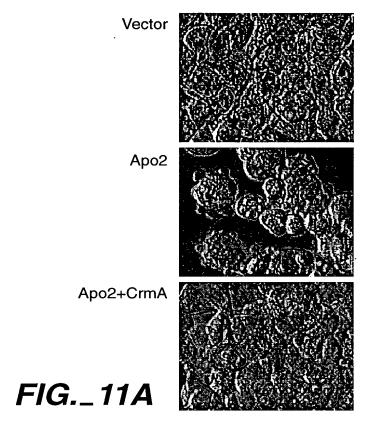
LAPQQRAAPQQKRSSPSEGLCPPGHHISEDGRDCIS<u>C</u>KYGQDYSTHWNDLLFCLRCTRCD SGEVELSPCTTTRNTVCQCEEGTFREEDSPEMCRKCRTGCPRGMVKVGDCTPWSDIECVH 61

KESGIIIGVTVAAVVLIVAVFVCKSLLWKKVLPYLKGICSGGGDPERVDRSSQRPGAED 181 121

NEGDPTETLRQCFDDFADLVPFDSW<u>EPLMRKLGLMDNEIKVAKAEAAGHRDTLYTMLIKW</u> <u>VNKTGRDASVHTLLDALFTLGERLAKQKIED</u>HLLSSGKFMYLEGNADSALS NVLNEIVSILOPTOVPEQEMEVQEPAEPTGVNMLSPGESEHLLEPAEAERSQRRRLLVPA 241

301

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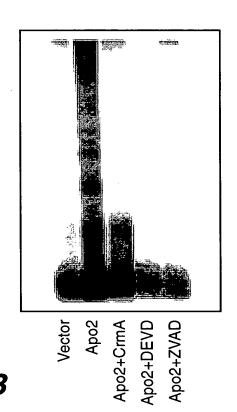
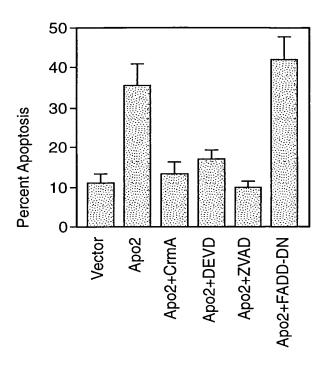


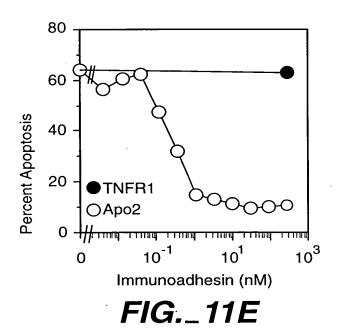
FIG._11B



Control
Apo2ECD
Apo2-IgG
Apo4-IgG
TNFR1-IgG

FIG._11C

FIG._11D



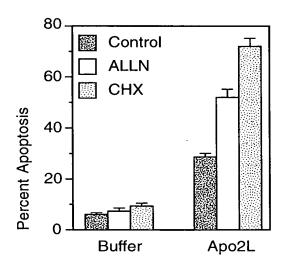
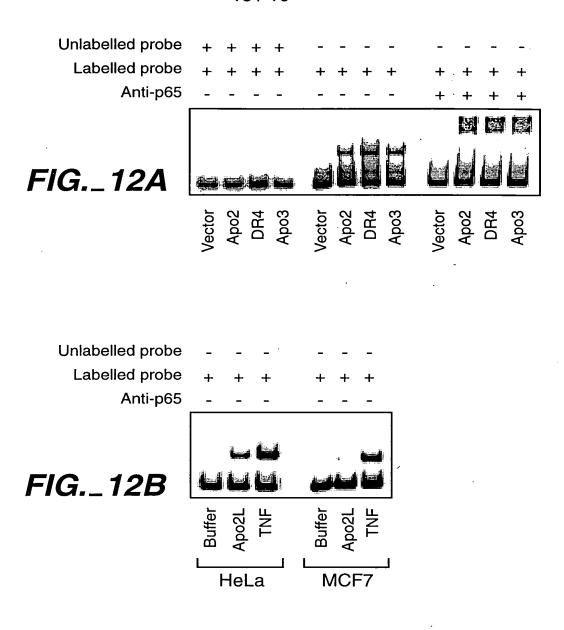


FIG._12C

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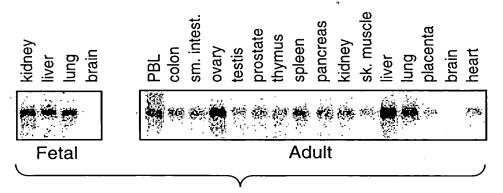


FIG._13

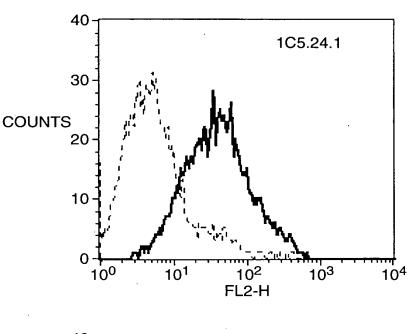


FIG._14A

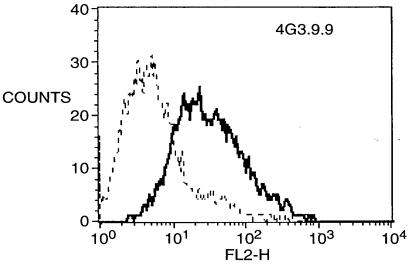


FIG._14B

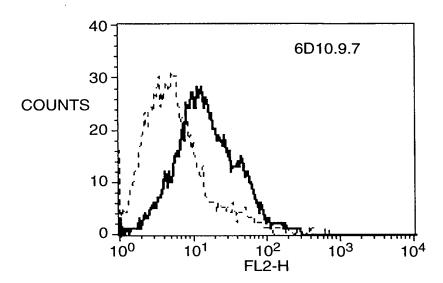


FIG._14C

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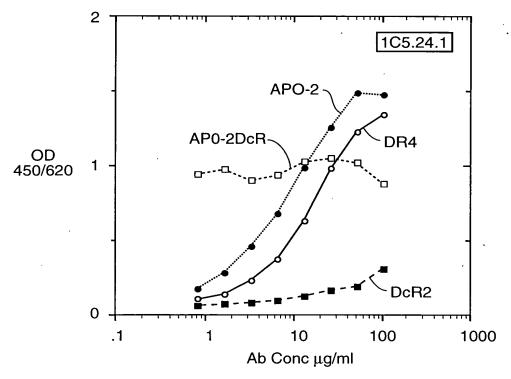


FIG._15A

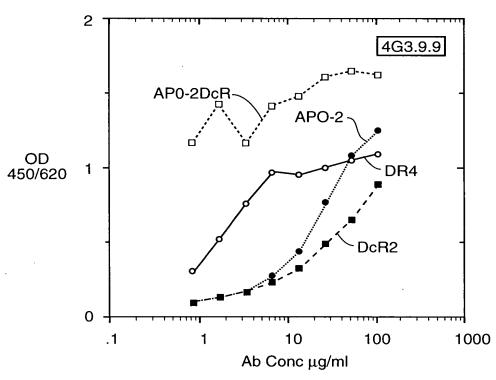


FIG._15B

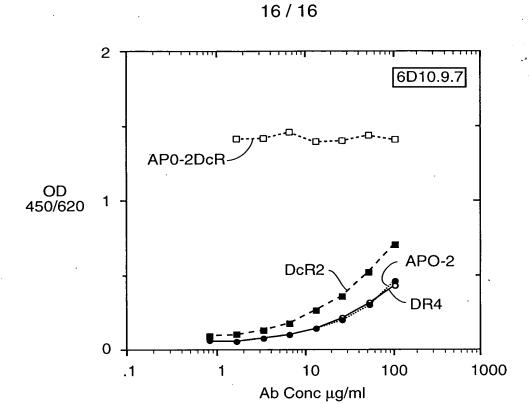


FIG._15C

Summary of mAbs to DcR1

mAbs	ISOTYPE	FACS		Cross reactivity		
		(HUMEC)	DR4	Apo-2	Apo-2DcR	DcR2
1C5.24.1	IgG1	+	++	+++	+++	-
4G3.9.9	IgG1	+	++	+	+++	+/-
6D10.9.7	IgG2b	+	_		+++	+/-

Percent Cross reactivity was determined by comparing the binding capacity to Apo-2DcR at 10 ug/ml of mAbs in ELISA. ++: >75% , +: 25-75%, +/-:10-25%, -: <10% .

FIG._16